

**The nucleotide sequence and deduced amino acid sequence of the genes for cytochrome  $c_L$  and a hypothetical second subunit of the methanol dehydrogenase of *Methylobacterium* AM1**

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Methanol dehydrogenase (MDH) is a periplasmic quinoprotein having cytochrome  $c_L$  as its electron acceptor (1,2). This cytochrome is specific for methanol oxidation, and its structural gene maps very close to that for MDH (1, 3). Although previously thought to consist of only two (identical) subunits ( $M_r$ , 60,000), MDH often shows an additional weakly-staining band ( $M_r$ , 8,000) on SDS-PAGE (4). During sequencing of DNA of *Methylobacterium* AM1 a protein-coding region (Mox I) was observed immediately adjacent to the structural gene for cytochrome  $c_L$  (Mox G). The nucleotide sequence of these two coding regions is presented below (in the order MoxG, MoxI), together with the deduced amino acid sequences. The leader sequences, termination triplets and haem-binding region are underlined. The first 10 amino acids of the *N*-terminal region of the purified protein 'contaminant' of the MDH correspond to the *N*-terminal region of the protein sequence derived from the Mox I gene. These results strongly suggest that what was previously thought to be a contaminant of methanol dehydrogenase is, in fact, a second type of subunit. The position of the haem-binding site (-C-S-G-C-H-) on the cytochrome  $c_L$  is clearly different from that in other Class I cytochromes *c*, in which it occurs within the first 20 residues.

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                                     M M N R V K I G T A L L G L
781  ACTTCGTCGGAAAGCGCTCTAAACGTGTGCTGAGGACCAAGAACAAGACGATGATGAACCGCGTAAAGATCGGAACCGCCCTTCTCGGCC
    T L A G I A L P A L A Q P Q S G P Q T G V V F R N T V T G E
871  TAACGCTCGCAGGCATTGCCCTGCCCGCGCTCGCCAGCCGCAATCCGGGCGCGACACCGCGCTCGTGTTCGCAACACCGTGACCGGCG
    A L D V S Q G K E G G R D T P A V K K F L E T G E N L Y I D
961  AGGCGCTCGACGTGTGCAAGGCAAGGAAGGCGCGCGACACGCCCGCGTGAAGAAGTTCTCGAGACCGCGGAGAACCTCTACATCG
    D K S C L R N G E S L F A T S C S G C H G H L A E G K L G P
1051 ACGACAAGTCCTGCTGCGGAATGGCGAGAGTCTGTTGCGGACGTCTTGCTCGGGCTGCCACGCCACCTCGCGAGGGCAAGCTCGGGC
    G L N D N Y W T Y P S N T T D V G L F A T I F G G A N G M M
1141 CGGGCTGAACACAATTACTGGACCTACCCGTCCAACACCACGATGTGGGCTGTTCGCCACGATCTTCGGCGGCGCCACGGCATGA
    G P H N E N L T P D E M L Q T I A W I R H L Y T G P K Q D A
1231 TGGGCCCGCACACGAGAATCTGACGCCGACGAGATGCTTCAGACCATCGCTGGATTTCGCCACCTCTATACGGGGCGAAGCAGGACG
    V W L N D E Q K K A Y T P Y K Q G E V I P K D A K G Q C K P
1321 CCGTCTGGCTCAACGACGACGAGAAGAAGCCCTACACGCCCTACAAGCAGGCGCAAGTCATCCGAAGGACGCCAAGGGCCAGTGAACG
    L D E
1411 CGCTGGACGAGTGAATCTTCGGGGTTTCGGGCGGGCTCGAACCGCGCGATCGAGGGGGCGGGATCGCCGCTCGCGACAAGTCCCAAGA
                                     M K T T L I A A A I V A L S G L A A P A L
1501  AGAGCAAGTCCCATAAAGTGAGGAAACATGAAGACCACTCTCATCGCCGCGCCGATCGTCGCCCTGTCCGGGCTCGCCGCCCCGGCGC
    A Y D G T K C K A A G N C W E P K P G F P E K I A G S K Y D
1591  TCGCCTATGACGGCACCAAGTGAAGGCCGCGGGCAATTGCTGGGAGCGGAAGCCCGCTTCCCGAGAAGATCGCCGGCTCCAAGTACG
    P K H D P K E L N K Q A D S I K Q M E E R N K K R V E N F K
1681  ATCCCAAGCAGATCCCAAGGAGCTGAACAAGCAGCGCGATTCCATCAAGCAGATGGAAGAGCGCAACAAGAAGCGTGTGAGAACTTCA
    K T G K F E Y D V A K I S A N
1771  AGAAGACCGCAAGTCAATACGACGTCGCAAGATTCGGCGAACTGATCCGCTGAGGCTCCGCCCTCTCCCTTCGGATCTCGGACCT
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